ABSTRACT

The present invention relates to a method for the detection and/or typing of *Helicobacter pylori* (*H. pylori*) strains present in a sample comprising the steps of: (i) if need be releasing, isolating or concentrating the polynucleic acids in the sample, (ii) amplifying the polynucleic acids of relevant target regions of the vacA gene and possibly other virulence determinant genes (VDG), with suitable primer pairs, said primers being generally applicable on different *H. pylori* strains, allowing to amplify said relevant target regions of the VDG preferentially in compatible amplification conditions; (iii) hybridizing the polynucleic acids obtained in (i) or (ii) with a set of at least two VDG-derived probes, under appropriate hybridization and wash conditions, and with at least one of said probes hybridizing to a conserved region of a VDG of *H. pylori*, and with at least one of said probes hybridizing to a variable region of vacA; (iv) detecting the hybrids formed in step (iii), (v) detecting and/or typing *H. pylori* strains present in a sample from the differential hybridization signals obtained in step (iv), with said typing being the allele-specific detection of a strain according to the VDG alleles present in that particular *H. pylori* strain, and the said virulence determinant genes being the genetic elements involved in enabling, determining, and marking of the infectivity and/or pathogenicity of said *H. pylori* strain. The present invention also relates to probes and primers for doing the same as well as *Helicobacter pylori* detecting/typing kits. The present invention also discloses novel sequences of VDG, which can be used for designing the above-mentioned primers and probes.